

SEQUENCE SUBMISSION

SEQ ID NO: 1 is human C23 nucleotide sequence.
SEQ ID NO: 2 is human C23 amino acid sequence.
SEQ ID NO: 3 is PCR primer for coding strand.
SEQ ID NO: 4 is PCR primer for noncoding strand.

10 (1) GENERAL INFORMATION:

(i) APPLICANT: Franz-Bacon, Karin
Gorman, Daniel M.
McClanahan, Terrill K.

(ii) TITLE OF INVENTION: MAMMALIAN GENES; RELATED REAGENTS

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US not yet assigned
(B) FILING DATE: 18-JUN-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/050,156
(B) FILING DATE: 17-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0744K

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-852-9196
(B) TELEFAX: 650-496-1200

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

Sub
aa
868190-868500

(D) TOPOLOGY: linear

~~(ii)~~ MOLECULE TYPE: cDNA

(ix) ~~FEATURE:~~

~~(A)~~ NAME/KEY: CDS

(B) LOCATION: 47..370

(ix) ~~FEATURE:~~

(A) NAME/KEY: mat_peptide

(B) LOCATION: 101..370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGTGCCGGA TTTGGTTAGC / TGAGCCCACC GAGAGGCGCC TGCAGG ATG AAA GCT 55
Met Lys Ala
-18

20 CTC TGT CTC CTC CTC CCT GTC CTG GGG CTG TTG GTG TCT AGC AAG 103
Leu Cys Leu Leu Leu Leu Pro Val Leu Gly Leu Leu Val Ser Ser Lys
-15 -10 -5 1

25 ACC CTG TGC TCC ATG GAA GAA GCC ATC AAT GAG AGG ATC CAG GAG GTC 151
Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile Gln Glu Val
5 10 15

30 GCC GGC TCC CTA ATA TTT AGG GCA ATA AGC AGC ATT GGC CTG GAG TGC 199
Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly Leu Glu Cys
20 25 30

35 CAG AGC GTC ACC TCC AGG GGG GAC CTG GCT ACT TGC CCC CGA GGC TTC 247
Gln Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro Arg Gly Phe
35 40 45

GCC GTC ACC GGC TGC ACT TGT GGC TCC GCC TGT GGC TCG TGG GAT GTG 295
Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser Trp Asp Val
50 55 60 65

CGC GCC GAG ACC ACA TGT CAC TGC CAG TGC GCG GGC ATG GAC TGG ACC 343
Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met Asp Trp Thr
70 75 80

45 GGA GCG CGC TGC TGT CGT GTG CAG CCC TGAGGTCGCG CGCAGCGCGT 390
Gly Ala Arg Cys Cys Arg Val Gln Pro
85 90

50 GCACAGCGCG GGC GGAGGCG GCTCCAGGTC CGAGGGGTT GCGGGGAGC TGGAAATAAA 450
CCT 453

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Ala Leu Cys Leu Leu Leu Leu Pro Val Leu Gly Leu Leu Val
-18 -15 -10 -5

10 Ser Ser Lys Thr Leu Cys Ser Met Glu Glu Ala Ile Asn Glu Arg Ile
1 5 10

Gln Glu Val Ala Gly Ser Leu Ile Phe Arg Ala Ile Ser Ser Ile Gly
15 20 25 30

15 Leu Glu Cys Gln Ser Val Thr Ser Arg Gly Asp Leu Ala Thr Cys Pro
35 40 45

20 Arg Gly Phe Ala Val Thr Gly Cys Thr Cys Gly Ser Ala Cys Gly Ser
50 55 60

Trp Asp Val Arg Ala Glu Thr Thr Cys His Cys Gln Cys Ala Gly Met
65 70 75

25 Asp Trp Thr Gly Ala Arg Cys Cys Arg Val Gln Pro
80 85 90

(2) INFORMATION FOR SEQ ID NO:3:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGTGGCTHYG SCTGTGGMTC KTGG

24

45 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

00099999-001000

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DX0744K

CAGCAGCGSG CWSHKETCSA GTC

23

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868190" 86866060